PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/471,749*

DATE: 03/31/2000
TIME: 09:44:10

INPUT SET: S35194.raw

#6

ENTERED

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
 1                              SEQUENCE LISTING
 2
 3   (1)    General Information:
 4
 5          (i) APPLICANT: Hillman, Jennifer L.
 6                         Corley, Neil C.
 7                         Guegler, Karl J.
 8                         Patterson, Chandra
 9                         Baughn, Mariah
10
11          (ii) TITLE OF INVENTION: HUMAN APOPTOSIS ASSOCIATED PROTEINS
12
13          (iii) NUMBER OF SEQUENCES: 12
14
15          (iv) CORRESPONDENCE ADDRESS:
16             (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
17             (B) STREET: 3174 Porter Dr.
18             (C) CITY: Palo Alto
19             (D) STATE: CA
20             (E) COUNTRY: USA
21             (F) ZIP: 94304
22
23          (v) COMPUTER READABLE FORM:
24             (A) MEDIUM TYPE: Diskette
25             (B) COMPUTER: IBM Compatible
26             (C) OPERATING SYSTEM: DOS
27             (D) SOFTWARE: FastSEQ for Windows Version 2.0
28
29          (vi) CURRENT APPLICATION DATA:
30             (A) APPLICATION NUMBER: 09/471,749
31             (B) FILING DATE:
32
33          (vii) PRIOR APPLICATION DATA:
34             (A) APPLICATION NUMBER:  09/078,402
35             (B) FILING DATE:
36
37         (viii) ATTORNEY/AGENT INFORMATION:
38             (A) NAME: Cerrone, Michael C.
39             (B) REGISTRATION NUMBER: 39,132
40             (C) REFERENCE/DOCKET NUMBER: PF-0519 US
41
42          (ix) TELECOMMUNICATION INFORMATION:
43             (A) TELEPHONE: 650-855-0555
44             (B) TELEFAX: 650-845-4166
45
46             (2) INFORMATION FOR SEQ ID NO:1:
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/471,749*

INPUT SET: S35194.raw

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47
48            (i) SEQUENCE CHARACTERISTICS:
49               (A) LENGTH: 480 amino acids
50               (B) TYPE: amino acid
51               (C) STRANDEDNESS: single
52               (D) TOPOLOGY: linear
53
54           (vii) IMMEDIATE SOURCE:
55               (A) LIBRARY: THP1PLB02
56               (B) CLONE: 157658
57
58            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
59
60
61    Met Ser Ala Glu Val Ile His Gln Val Glu Glu Ala Leu Asp Thr Asp
62     1               5                  10                  15
63    Glu Lys Glu Met Leu Leu Phe Leu Cys Arg Asp Val Ala Ile Asp Val
64             20                  25                  30
65    Val Pro Pro Asn Val Arg Asp Leu Leu Asp Ile Leu Arg Glu Arg Gly
66             35                  40                  45
67    Lys Leu Ser Val Gly Asp Leu Ala Glu Leu Leu Tyr Arg Val Arg Arg
68         50                  55                  60
69    Phe Asp Leu Leu Lys Arg Ile Leu Lys Met Asp Arg Lys Ala Val Glu
70    65                  70                  75                  80
71    Thr His Leu Leu Arg Asn Pro His Leu Val Ser Asp Tyr Arg Val Leu
72                 85                  90                  95
73    Met Ala Glu Ile Gly Glu Asp Leu Asp Lys Ser Asp Val Ser Ser Leu
74                 100                 105                 110
75    Ile Phe Leu Met Lys Asp Tyr Met Gly Arg Gly Lys Ile Ser Lys Glu
76             115                 120                 125
77    Lys Ser Phe Leu Asp Leu Val Val Glu Leu Glu Lys Leu Asn Leu Val
78         130                 135                 140
79    Ala Pro Asp Gln Leu Asp Leu Leu Glu Lys Cys Leu Lys Asn Ile His
80    145                 150                 155                 160
81    Arg Ile Asp Leu Lys Thr Lys Ile Gln Lys Tyr Lys Gln Ser Val Gln
82                 165                 170                 175
83    Gly Ala Gly Thr Ser Tyr Arg Asn Val Leu Gln Ala Ala Ile Gln Lys
84                 180                 185                 190
85    Ser Leu Lys Asp Pro Ser Asn Asn Phe Arg Leu His Asn Gly Arg Ser
86             195                 200                 205
87    Lys Glu Gln Arg Leu Lys Glu Gln Leu Gly Ala Gln Gln Glu Pro Val
88         210                 215                 220
89    Lys Lys Ser Ile Gln Glu Ser Glu Ala Phe Leu Pro Gln Ser Ile Pro
90    225                 230                 235                 240
91    Glu Glu Arg Tyr Lys Met Lys Ser Lys Pro Leu Gly Ile Cys Leu Ile
92                 245                 250                 255
93    Ile Asp Cys Ile Gly Asn Glu Thr Glu Leu Leu Arg Asp Thr Phe Thr
94                 260                 265                 270
95    Ser Leu Gly Tyr Glu Val Gln Lys Phe Leu His Leu Ser Met His Gly
96             275                 280                 285
97    Ile Ser Gln Ile Leu Gly Gln Phe Ala Cys Met Pro Glu His Arg Asp
98             290                 295                 300
99    Tyr Asp Ser Phe Val Cys Val Leu Val Ser Arg Gly Gly Ser Gln Ser
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INPUT SET: S35194.raw

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100   305                   310                   315                   320
101   Val Tyr Gly Val Asp Gln Thr His Ser Gly Leu Pro Leu His His Ile
102                         325                   330                   335
103   Arg Arg Met Phe Met Gly Asp Ser Cys Pro Tyr Leu Ala Gly Lys Pro
104                   340                   345                   350
105   Lys Met Phe Phe Ile Gln Asn Tyr Val Val Ser Glu Gly Gln Leu Glu
106             355                   360                   365
107   Asp Ser Ser Leu Leu Glu Val Asp Gly Pro Ala Met Lys Asn Val Glu
108         370                   375                   380
109   Phe Lys Ala Gln Lys Arg Gly Leu Cys Thr Val His Arg Glu Ala Asp
110   385                   390                   395                   400
111   Phe Phe Trp Ser Leu Cys Thr Ala Asp Met Ser Leu Leu Glu Gln Ser
112                   405                   410                   415
113   His Ser Ser Pro Ser Leu Tyr Leu Gln Cys Leu Ser Gln Lys Leu Arg
114                   420                   425                   430
115   Gln Glu Arg Lys Arg Pro Leu Leu Asp Leu His Ile Glu Leu Asn Gly
116             435                   440                   445
117   Tyr Met Tyr Asp Trp Asn Ser Arg Val Ser Ala Lys Glu Lys Tyr Tyr
118         450                   455                   460
119   Val Trp Leu Gln His Thr Leu Arg Lys Lys Leu Ile Leu Ser Tyr Thr
120   465                   470                   475                   480
121
122             (2) INFORMATION FOR SEQ ID NO:2:
123
124         (i) SEQUENCE CHARACTERISTICS:
125             (A) LENGTH: 2352 base pairs
126             (B) TYPE: nucleic acid
127             (C) STRANDEDNESS: single
128             (D) TOPOLOGY: linear
129
130         (vii) IMMEDIATE SOURCE:
131             (A) LIBRARY: THP1PLB02
132             (B) CLONE: 157658
133
134         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
135
136   GAAATTGCGC CACTGCACTC CAGCCTGGGC CACAGAGCGA GACTCTGTCT CAAAAAAGAA      60
137   GGAAAGAAAG AAAGAAAAAA AAAAACACTC GCAGTGTTTA CTCCTAACGC GTGGAACTTG     120
138   TGTCGACATC CACCCCCGGT TACTGCATAC TCAGTCACAC AAGCCATAGC AGGAAACAGC     180
139   GAGCTTGCAG CCTCACCGAC GAGTCTCAAC TAAAAGGGAC TCCCGGAGCT AGGGGTGGGG     240
140   ACTCGGCCTC ACACAGTGAG TGCCGGCTAT TGGACTTTTG TCCAGTGACA GCTGAGACAA     300
141   CAAGGACCAC GGGAGGAGGT GTAGGAGAGA AGCGCCGCGA ACAGCGATCG CCCAGCACCA     360
142   AGTCCGCTTC CAGGCTTTCG GTTTCTTTGC CTCCATCTTG GGTGCGCCTT CCCGGCGTCT     420
143   AGGGGAGCGA AGGCTGAGGT GGCAGCGGCA GGAGAGTCCG GCCGCGACAG GACGAACTCC     480
144   CCCACTGGAA AGGATTCTGA AAGAAATGAA GTCAGCCCTC AGAAATGAAG TTGACTGCCT     540
145   GCTGGCTTTC TGTTGACTGG CCCGGAGCTG TACTGCAAGA CCCTTGTGAG CTTCCCTAGT     600
146   CTAAGAGTAG GATGTCTGCT GAAGTCATCC ATCAGGTTGA AGAAGCACTT GATACAGATG     660
147   AGAAGGAGAT GCTGCTCTTT TTGTGCCGGG ATGTTGCTAT AGATGTGGTT CCACCTAATG     720
148   TCAGGGACCT TCTGGATATT TTACGGGAAA GAGGTAAGCT GTCTGTCGGG GACTTGGCTG     780
149   AACTGCTCTA CAGAGTGAGG CGATTTGACC TGCTCAAACG TATCTTGAAG ATGGACAGAA     840
150   AAGCTGTGGA GACCCACCTG CTCAGGAACC CTCACCTTGT TTCGGACTAT AGAGTGCTGA     900
151   TGGCAGAGAT TGGTGAGGAT TTGGATAAAT CTGATGTGTC CTCATTAATT TTCCTCATGA     960
152   AGGATTACAT GGGCCGAGGC AAGATAAGCA AGGAGAAGAG TTTCTTGGAC CTTGTGGTTG    1020
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INPUT SET: S35194.raw

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153   AGTTGGAGAA ACTAAATCTG GTTGCCCCAG ATCAACTGGA TTTATTAGAA AAATGCCTAA   1080
154   AGAACATCCA CAGAATAGAC CTGAAGACAA AAATCCAGAA GTACAAGCAG TCTGTTCAAG   1140
155   GAGCAGGGAC AAGTTACAGG AATGTTCTCC AAGCAGCAAT CCAAAAGAGT CTCAAGGATC   1200
156   CTTCAAATAA CTTCAGGCTC CATAATGGGA GAAGTAAAGA ACAAAGACTT AAGGAACAGC   1260
157   TTGGCGCTCA ACAAGAACCA GTGAAGAAAT CCATTCAGGA ATCAGAAGCT TTTTTGCCTC   1320
158   AGAGCATACC TGAAGAGAGA TACAAGATGA AGAGCAAGCC CCTAGGAATC TGCCTGATAA   1380
159   TCGATTGCAT TGGCAATGAG ACAGAGCTTC TTCGAGACAC CTTCACTTCC CTGGGCTATG   1440
160   AAGTCCAGAA ATTCTTGCAT CTCAGTATGC ATGGTATATC CCAGATTCTT GGCCAATTTG   1500
161   CCTGTATGCC CGAGCACCGA GACTACGACA GCTTTGTGTG TGTCCTGGTG AGCCGAGGAG   1560
162   GCTCCCAGAG TGTGTATGGT GTGGATCAGA CTCACTCCGG GCTCCCCCTG CATCACATCA   1620
163   GGAGGATGTT CATGGGAGAT TCATGCCCTT ATCTAGCAGG GAAGCCAAAG ATGTTTTTTA   1680
164   TTCAGAACTA TGTGGTGTCA GAGGGCCAGC TGGAGGACAG CAGCCTCTTG GAGGTGGATG   1740
165   GGCCAGCGAT GAAGAATGTG GAATTCAAGG CTCAGAAGCG AGGGCTGTGC ACAGTTCACC   1800
166   GAGAAGCTGA CTTCTTCTGG AGCCTGTGTA CTGCGGACAT GTCCCTGCTG GAGCAGTCTC   1860
167   ACAGCTCACC ATCCCTGTAC CTGCAGTGCC TCTCCCAGAA ACTGAGACAA GAAAGAAAAC   1920
168   GCCCACTCCT GGATCTTCAC ATTGAACTCA ATGGCTACAT GTATGATTGG AACAGCAGAG   1980
169   TTTCTGCCAA GGAGAAATAT TATGTCTGGC TGCAGCACAC TCTGAGAAAG AAACTTATCC   2040
170   TCTCCTACAC ATAAGAAACC AAAAGGCTGG GCGTAGTGGC TCACACCTGT GATCCCAGCA   2100
171   CTTTGGGAGG CCAAGGAGGG CAGATCACTT CAGGTCAGGA GTTCGAGACC AGCCTGGCCA   2160
172   ACATGGTAAA CGCTGTCCCT AGTAAAAATA CAAAAATTAG CTGGGTGTGG GTGTGGGTAC   2220
173   CTGTATTCCC AGTTACTTGG GAGGCTGAGG TGGGAGGATC TTTTGAACCC AGGAGTTCAG   2280
174   GGTCATAGCA TGCTGTGATT GTGCCTACGA ATAGCCACTG CATACCAACC TGGGCAATAT   2340
175   AGCAAGATCC CA                                                        2352
176
177           (2) INFORMATION FOR SEQ ID NO:3:
178
179           (i) SEQUENCE CHARACTERISTICS:
180               (A) LENGTH: 238 amino acids
181               (B) TYPE: amino acid
182               (C) STRANDEDNESS: single
183               (D) TOPOLOGY: linear
184
185           (vii) IMMEDIATE SOURCE:
186               (A) LIBRARY: BRSTNOT03
187               (B) CLONE: 642272
188
189           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
190
191   Met Glu Tyr Ala Met Lys Ser Leu Ser Leu Leu Tyr Pro Lys Ser Leu
192    1               5                  10                  15
193   Ser Arg His Val Ser Val Arg Thr Ser Val Val Thr Gln Gln Leu Leu
194            20                  25                  30
195   Ser Glu Pro Ser Pro Lys Ala Pro Arg Ala Arg Pro Cys Arg Val Ser
196            35                  40                  45
197   Thr Ala Asp Arg Ser Val Arg Lys Gly Ile Met Ala Tyr Ser Leu Glu
198            50                  55                  60
199   Asp Leu Leu Leu Lys Val Arg Asp Thr Leu Met Leu Ala Asp Lys Pro
200   65                  70                  75                  80
201   Phe Phe Leu Val Leu Glu Glu Asp Gly Thr Thr Val Glu Thr Glu Glu
202            85                  90                  95
203   Tyr Phe Gln Ala Leu Ala Gly Asp Thr Val Phe Met Val Leu Gln Lys
204            100                 105                 110
205   Gly Gln Lys Trp Gln Pro Pro Ser Glu Gln Gly Thr Arg His Pro Leu
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INPUT SET: S35194.raw

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206              115                   120                   125
207   Ser Leu Ser His Lys Pro Ala Lys Lys Ile Asp Val Ala Arg Val Thr
208        130                   135                   140
209   Phe Asp Leu Tyr Lys Leu Asn Pro Gln Asp Phe Ile Gly Cys Leu Asn
210   145                   150                   155                   160
211   Val Lys Ala Thr Phe Tyr Asp Thr Tyr Ser Leu Ser Tyr Asp Leu His
212                   165                   170                   175
213   Cys Cys Gly Ala Lys Arg Ile Met Lys Glu Ala Phe Arg Trp Ala Leu
214                   180                   185                   190
215   Phe Ser Met Gln Ala Thr Gly His Val Leu Leu Gly Thr Ser Cys Tyr
216             195                   200                   205
217   Leu Gln Gln Leu Leu Asp Ala Thr Glu Glu Gly Gln Pro Pro Lys Gly
218        210                   215                   220
219   Lys Ala Ser Ser Leu Ile Pro Thr Cys Leu Lys Ile Leu Gln
220   225                   230                   235
221
222            (2) INFORMATION FOR SEQ ID NO:4:
223
224        (i) SEQUENCE CHARACTERISTICS:
225           (A) LENGTH: 1284 base pairs
226           (B) TYPE: nucleic acid
227           (C) STRANDEDNESS: single
228           (D) TOPOLOGY: linear
229
230        (vii) IMMEDIATE SOURCE:
231           (A) LIBRARY: BRSTNOT03
232           (B) CLONE: 642272
233
234        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
235
236   AATGTTCTTT TGGCCACTGT GAAGCCTCAG GAAGGGGCTC GGATTGCTCA AGGACCCATG     60
237   GGAGAGAGGA GGCTTTGACT GGGCTGCCTG CCTGTGAGGT CTCTGGACTA GAGGTCCAAC    120
238   GCAGTCCAGC TGACAAGGAT GGAATACGCC ATGAAGTCCC TTAGCCTTCT CTACCCCAAG    180
239   TCCCTCTCCA GGCATGTGTC AGTGCGTACC TCTGTGGTGA CCCAGCAGCT GCTGTCGGAG    240
240   CCCAGCCCCA AGGCCCCCAG GGCCCGGCCC TGCCGCGTAA GCACGGCGGA TCGAAGCGTG    300
241   AGGAAGGGCA TCATGGCTTA CAGTCTTGAG GACCTCCTCC TCAAGGTCCG GGACACTCTG    360
242   ATGCTGGCAG ACAAGCCCTT CTTCCTGGTG CTGGAGGAAG ATGGCACAAC TGTAGAGACA    420
243   GAAGAGTACT TCCAAGCCCT GGCAGGGGAT ACAGTGTTCA TGGTCCTCCA GAAGGGGCAG    480
244   AAATGGCAGC CCCCATCAGA ACAGGGGACA AGGCACCCAC TGTCCCTCTC CCATAAGCCT    540
245   GCCAAGAAGA TTGATGTGGC CCGTGTAACG TTTGATCTGT ACAAGCTGAA CCCACAGGAC    600
246   TTCATTGGCT GCCTGAACGT GAAGGCGACT TTTTATGATA CATACTCCCT TTCCTATGAT    660
247   CTGCACTGCT GTGGGGCCAA GCGCATCATG AAGGAAGCTT TCCGCTGGGC CCTCTTCAGC    720
248   ATGCAGGCCA CAGGCCACGT ACTGCTTGGC ACCTCCTGTT ACCTGCAGCA GCTCCTCGAT    780
249   GCTACGGAGG AAGGGCAGCC CCCCAAGGGC AAGGCCTCAT CCCTTATCCC GACCTGTCTG    840
250   AAGATACTGC AGTGAAAGCC CAAGTCCTTG GAAGCTTTCC CCAGTGAAGG ACTGACTGGG    900
251   GGCCTCACGC TTAACTGGTA GTGCCCACAA GCCTGGCAGC TGTAGAGCCG CGAACCTCCC    960
252   CACACCTCCC TCACCGCGCA GGACCCTGAG TGAGGAGGAG GAGCTGGAAA CCTGGGGTGG   1020
253   GTTGGCCAAA GGAGAACCTC AAGCTCCTGG CCTGATCCAG CTCCTTCCTG CCCAAGGCAG   1080
254   CTTAGCCCAT CCAGACTGGT CCTGAAGTCT GTCCCTCCAT TGGCATGAAG TCTGCCCCTT   1140
255   AGCAATCCGG CCTCGCAGGC TGTACTTTCA TGGTGCTCTC TACCTTCTGG CCCCCATCCC   1200
256   GGAACATTCC TGAGTGAATT CGCAAGCGCA CTAGCATGTG ATATTAGGGA GTTTGCAATA   1260
257   AATTATTGAG GCTGAAAAAA AAAA                                         1284
258
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/09/471,749*

INPUT SET: S35194.raw

Line   Error   Original Text